Amendments to the Specification:

Please amend the specification as follows:

Page 1, please insert the following paragraph immediately subsequent to the title.

This application is the National Stage of International Application No. PCT/US00/19980, filed July 20, 2000, which claims the benefit of U.S. Provisional Application No. 60/144,992, filed July 22, 1999 and U.S. Provisional Application No. 60/168,858, filed December 2, 1999.

Please replace paragraph starting at page 15, line 5 with the following rewritten paragraph:

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on ~~the Internet at http://www.ncbi.nlm.nih.gov/BLAST/~~NCBI's web site. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at ~~http://www.ncbi.nlm.nih.gov/gorf/bl2.html~~ the National Center for Biotechnology Information web site. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62
Reward for match: 1
Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Please replace paragraph starting at page 51, line 15 with the following rewritten paragraph:

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanism, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000~~, available at http://www.niehs.nih.gov/oc/news/toxchip.htm.~~) Therefor it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

Please replace paragraph starting at page 60, line 22 with the following rewritten paragraph:

The genetic map locations of SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 21, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, and SEQ ID NO: 30 are described in The Invention as ranges, or intervals, of human chromosomes. More than one map location is reported for SEQ ID NO: 28 and SEQ ID NO: 29, indicating that previously mapped sequences having similarity, but not complete identity, to SEQ ID NO: 28 and SEQ ID NO: 29 were assembled into their respective clusters. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Diseases associated with the public and Incyte sequences located within the indicated intervals are also reported in the Invention where applicable. Human genome maps and other resources available to the public, such as the NCBI "GeneMap '99" World Wide Web site ~~which can be accessed at http://www.ncbi.nlm.nih.gov/genemap~~, can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.